

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANTS: Hansen, Peter Kamp
Wagner, Peter
Mullertz, Anette
Knap, Inge Helmer
- (ii) TITLE OF THE INVENTION: Animal Feed Additives
- (iii) NUMBER OF SEQUENCES: 2
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Novo Nordisk of North America, Inc.
 - (B) STREET: 405 Lexington Avenue
 - (C) CITY: New York
 - (D) STATE: NY
 - (E) COUNTRY: USA
 - (F) ZIP: 10174
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: to be assigned
 - (B) FILING DATE: 1-JUL-1997
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Lambiris, Elias J
 - (B) REGISTRATION NUMBER: 33,728
 - (C) REFERENCE/DOCKET NUMBER: 4324.204-US
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 212-867-0123
 - (B) TELEFAX: 212-878-9655

(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 983 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Thermomyces lanuginosus*
 - (B) STRAIN: DSM 4109
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 31..705
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

TCGGCCCGAC GTCTTGCAAT CCTTGCAAGT ATG GTC GGC TTT ACC CCC GTT GCC
Met Val Gly Phe Thr Pro Val Ala
1 5

54

CTT GCG GCC TTA GCC GCG ACT GGG GCC CTG GCC TTC CCG GCA GGG AAT Leu Ala Ala Leu Ala Ala Thr Gly Ala Leu Ala Phe Pro Ala Gly Asn 10 15 20	102
GCC ACG GAG CTC GAA AAG CGA CAG ACA ACC CCC AAC TCG GAG GGC TGG Ala Thr Glu Leu Glu Lys Arg Gln Thr Thr Pro Asn Ser Glu Gly Trp 25 30 35 40	150
CAC GAT GGT TAT TAC TAT TCC TGG TGG AGT GAC GGT GGA GCG CAG GCC His Asp Gly Tyr Tyr Tyr Ser Trp Trp Ser Asp Gly Gly Ala Gln Ala 45 50 55	198
ACG TAC ACC AAC CTG GAA GGC GGC ACC TAC GAG ATC AGC TGG GGA GAT Thr Tyr Thr Asn Leu Glu Gly Gly Thr Tyr Glu Ile Ser Trp Gly Asp 60 65 70	246
GGC GGT AAC CTC GTC GGT GGA AAG GGC TGG AAC CCC GGC CTG AAC GCA Gly Gly Asn Leu Val Gly Gly Lys Gly Trp Asn Pro Gly Leu Asn Ala 75 80 85	294
AGA GCC ATC CAC TTT GAG GGT GTT TAC CAG CCA AAC GGC AAC AGC TAC Arg Ala Ile His Phe Glu Gly Val Tyr Gln Pro Asn Gly Asn Ser Tyr 90 95 100	342
CTT GCG GTC TAC GGT TGG ACC CGC AAC CCG CTG GTC GAG TAT TAC ATC Leu Ala Val Tyr Gly Trp Thr Arg Asn Pro Leu Val Glu Tyr Tyr Ile 105 110 115 120	390
GTC GAG AAC TTT GGC ACC TAT GAT CCT TCC TCC GGT GCT ACC GAT CTA Val Glu Asn Phe Gly Thr Tyr Asp Pro Ser Ser Gly Ala Thr Asp Leu 125 130 135	438
GGA ACT GTC GAG TGC GAC GGT AGC ATC TAT CGA CTC GGC AAG ACC ACT Gly Thr Val Glu Cys Asp Gly Ser Ile Tyr Arg Leu Gly Lys Thr Thr 140 145 150	486
CGC GTC AAC GCA CCT AGC ATC GAC GGC ACC CAA ACC TTC GAC CAA TAC Arg Val Asn Ala Pro Ser Ile Asp Gly Thr Gln Thr Phe Asp Gln Tyr 155 160 165	534
TGG TCG GTC CGC CAG GAC AAG CGC ACC AGC GGT ACC GTC CAG ACG GGC Trp Ser Val Arg Gln Asp Lys Arg Thr Ser Gly Thr Val Gln Thr Gly 170 175 180	582
TGC CAC TTC GAC GCC TGG GCT CGC GCT GGT TTG AAT GTC AAC GGT GAC Cys His Phe Asp Ala Trp Ala Arg Ala Gly Leu Asn Val Asn Gly Asp 185 190 195 200	630
CAC TAC TAC CAG ATC GTT GCA ACG GAG GGC TAC TTC AGC AGC GGC TAT His Tyr Tyr Gln Ile Val Ala Thr Glu Gly Tyr Phe Ser Ser Gly Tyr 205 210 215	678
GCT CGC ATC ACC GTT GCT GAC GTG GGC TAAGACGTAA CCTGGTGGTG Ala Arg Ile Thr Val Ala Asp Val Gly 220 225	725
ATCTCGCGAG GCAACAGCCA AGAATGTCGT CAGATGTGCC GGTGAAGGT ATTCAATCAG	785
CATATCTGTC TGCCCTTGCG AGTGATACTT TGGAGGACTG TGGAGAACTT TGTGCGAGCC	845
TGGCCAGGAT CAGTAGTTGC TTTGCGGTGT TTTGCTCCCT ATTCTCGTGA AAAAATTGTT	905
ATTGCTTCGT TGTCTAGTGT ACATAGCCGA GCAATTGAGG CCTCACGCTT GGGAAAAAAA	965
AAAAAAAAAA AAAAAAAAAA	983

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Val Gly Phe Thr Pro Val Ala Leu Ala Ala Leu Ala Ala Thr Gly
1 5 10 15
Ala Leu Ala Phe Pro Ala Gly Asn Ala Thr Glu Leu Glu Lys Arg Gln
20 25 30
Thr Thr Pro Asn Ser Glu Gly Trp His Asp Gly Tyr Tyr Tyr Ser Trp
35 40 45
Trp Ser Asp Gly Gly Ala Gln Ala Thr Tyr Thr Asn Leu Glu Gly Gly
50 55 60
Thr Tyr Glu Ile Ser Trp Gly Asp Gly Gly Asn Leu Val Gly Gly Lys
65 70 75 80
Gly Trp Asn Pro Gly Leu Asn Ala Arg Ala Ile His Phe Glu Gly Val
85 90 95
Tyr Gln Pro Asn Gly Asn Ser Tyr Leu Ala Val Tyr Gly Trp Thr Arg
100 105 110
Asn Pro Leu Val Glu Tyr Tyr Ile Val Glu Asn Phe Gly Thr Tyr Asp
115 120 125
Pro Ser Ser Gly Ala Thr Asp Leu Gly Thr Val Glu Cys Asp Gly Ser
130 135 140
Ile Tyr Arg Leu Gly Lys Thr Thr Arg Val Asn Ala Pro Ser Ile Asp
145 150 155 160
Gly Thr Gln Thr Phe Asp Gln Tyr Trp Ser Val Arg Gln Asp Lys Arg
165 170 175
Thr Ser Gly Thr Val Gln Thr Gly Cys His Phe Asp Ala Trp Ala Arg
180 185 190
Ala Gly Leu Asn Val Asn Gly Asp His Tyr Tyr Gln Ile Val Ala Thr
195 200 205
Glu Gly Tyr Phe Ser Ser Gly Tyr Ala Arg Ile Thr Val Ala Asp Val
210 215 220
Gly
225